

Hong et al. – Serial No. 09/512,019
Amdt. dated February 24, 2004
Reply to Office Action of August 26, 2003
and Advisory Action dated February 5, 2004

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

Claims 1-8 (cancel without prejudice or disclaimer).

Claim 9 (currently amended). A host cell which produces a modified DNA polymerase having ~~[[an]] the amino acid sequence that shares not less than 95% homology to of SEQ ID NO:4, which DNA polymerase during DNA sequencing effectively incorporated fluorescent dye-labeled dideoxynucleotide terminators ddCTP, ddATP, ddTTP and ddGTP, and has a reduction in the selective discrimination against incorporation of fluorescent dye-labeled dideoxynucleotide terminators ddCTP and ddATP,~~

~~wherein the DNA polymerase in its unmodified state has leucine, glutamate, and glutamate residues at positions 342-344, respectively, and a phenylalanine at position 422, the positions being determined based on a last lysine residue in the end of the sequence counted as position 588, wherein the DNA polymerase selectively discriminates against incorporation of fluorescent dye-labeled dideoxynucleotide terminators ddCTP and ddATP but does not discriminate against incorporation of fluorescent dye-labeled dideoxynucleotide terminators ddTTP and ddGTP.~~

Claim 10 (original). The host cell according to claim 9, wherein the modified DNA polymerase has proofreading 3'-5' exonuclease activity during DNA sequencing of a DNA strand from a template, such that the DNA polymerase functions to excise mismatched nucleotides from the 3' terminus of the DNA strand at a faster rate than the rate at which the DNA polymerase functions to remove nucleotides matched correctly with nucleotides of the template.

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Claim 11 (cancel without prejudice or disclaimer).

Claim 12 (original). The host cell according to claim 9, wherein the DNA polymerase is encoded by nucleotide sequence SEQ ID NO:3.

Claim 13 (original). The host cell of claim 9, which is E. coli.

Claims 14-28 (cancel without prejudice or disclaimer).

Claim 29. (Amended) A DNA construct comprising:

- (i) a nucleotide sequence encoding a modified DNA polymerase which has an amino acid sequence that shares not less than 95% homology to a DNA polymerase isolated from a strain of *Bacillus stearothermophilus* of *Bacillus caldotenax*, having an amino acid sequence that shares not less than 95% homology to SEQ ID NO:4, which wherein said nucleotide sequence encodes threonine, proline and leucine residues at positions corresponding to positions 342-344, respectively, and a tyrosine residue at a position corresponding to position 422, wherein the DNA polymerase in its unmodified state has leucine, glutamate, and glutamate residues at positions 342-344, respectively, and a phenylalanine at position 422, the positions being determined based on a last lysine residue in the end of the sequence counted as position 588; and
- (ii) a vector, for introducing the DNA construct into eukaryotic and procaryotic host cells.

Claim 30 (original). The DNA construct according to claim 29 wherein the vector is a cloning vector or an expression vector.

Claims 31-38 (cancel without prejudice or disclaimer).

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Claim 39. (Amended) A modified nucleotide sequence encoding a DNA polymerase which has an amino acid sequence that shares not less than 95% homology to ~~a DNA polymerase isolated from a strain of *Bacillus stearothermophilus* or *Bacillus caldotenax*, having an amino acid sequence that shares not less than 95% homology to SEQ ID NO:4,~~ which wherein said nucleotide sequence encodes threonine, proline and leucine residues at positions corresponding to positions 342-344, respectively, and a tyrosine residue at a position corresponding to position 422, ~~wherein the DNA polymerase in its unmodified state has leucine, glutamate, and glutamate residues at positions 342-344, respectively, and a phenylalanine at position 422, the positions being determined based on a last lysine residue in the end of the sequence counted as position 588.~~

Claim 40. (previously amended) The modified nucleotide sequence according to claim 39 which has the nucleotide sequence of SEQ ID NO:3.

Claims 41-56 (cancel without prejudice or disclaimer).